Rapid deployment of a Machine Learning-based derived biomarker using publicly available data sources for covariate adjusted descriptive modeling.

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INTRODUCTION

Defining baseline characteristics for covariate-adjusted analyses to increase study power is not new. Multifactorial heterogeneous diseases including Amyotrophic Lateral Sclerosis (ALS), Alzheimer's Disease (AD), Parkinson's Disease (PD), and Huntington's Disease (HD) present a challenge in defining baseline covariates that add substantial benefit to study power. We developed a methodology for training machine-learning (ML) models that utilizes historical clinical trial patient data to provide a single prediction value to be used as a covariate in a trial's statistical analysis. We have adapted this methodology across disease areas and have developed a rigorous audit methodology based on best practices in the biostatistics field so that these new methods can be more easily shared across a field where rigorous vetting of new technologies is critical to adoption.

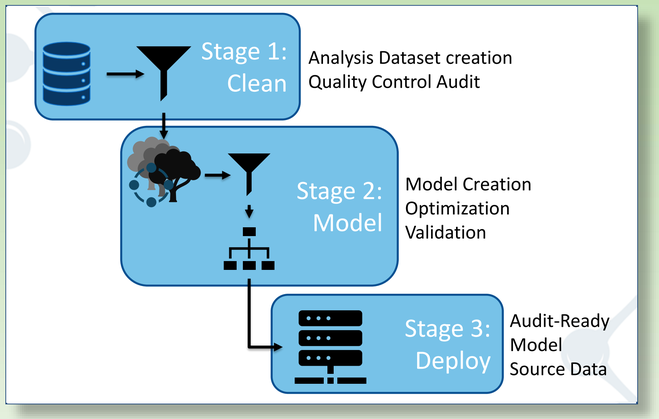
OBJECTIVE

To demonstrate through clinical trial simulation:

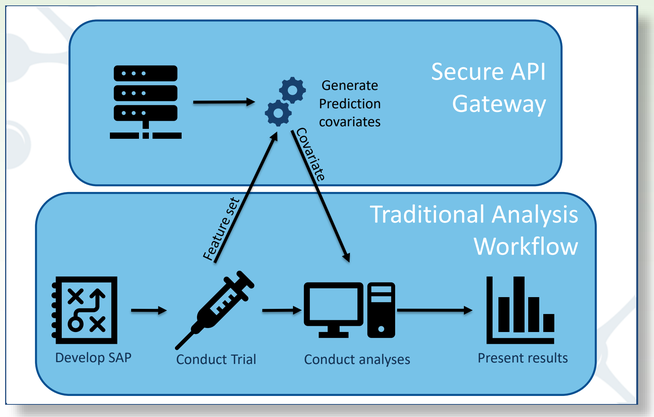
- A methodology for adopting rigorous methods for analysis dataset preparation for ML modeling
- A practical application of ML models to traditional biostatistical analysis
- A scalable approach that is applicable to multiple heterogeneous disease areas in which a suitable covariate is lacking

APPROACH

Standardized Workflow for Developing Machine Learning Models from Disease-Specific Clinical Trial Databases



Clinical Trial Workflow with ML Covariate Adjustment



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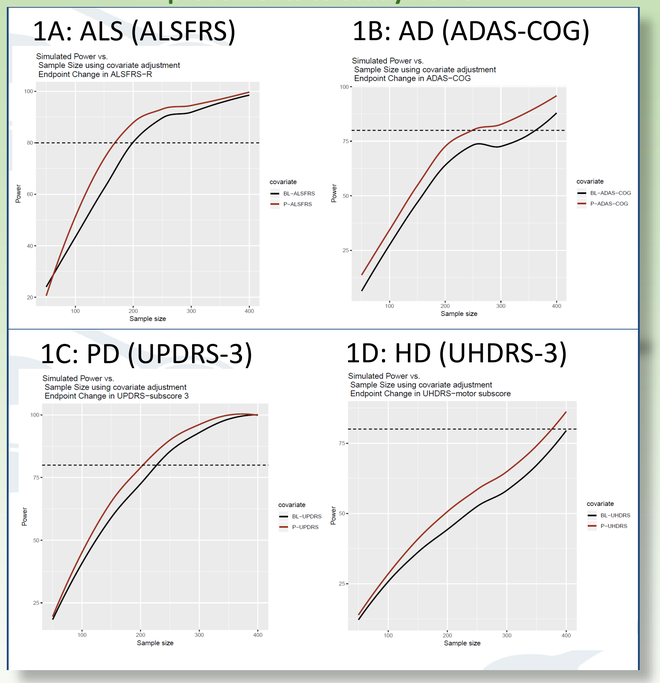
SIMULATION RESULTS

Clinical Trial Power Simulations Reveal Consistent Improvements to Study Power



Improvement to Study Power and reduction in variance (N = 150).

	ALS	AD	PD	HD
Power Boost	27.6%	26.2%	14.8%	20.6%
MSE Reduction	-18.1%	-11.7%	-3.6%	-10.2%

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